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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/461,646

DATE: 12/26/2000

TIME: 14:17:03

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3 <110> APPLICANT: Fibrogen, Inc.
4   Grotendorst, Gary
5   Neff, Thomas
7 <120> TITLE OF INVENTION: Connective Tissue Growth Factor Fragments and Methods and Uses Thereof
9 <130> FILE REFERENCE: FIBRO1130-2
11 <140> CURRENT APPLICATION NUMBER: 09/461,646
12 <141> CURRENT FILING DATE: 1999-12-14
14 <150> PRIOR APPLICATION NUMBER: 60/112,240
15 <151> PRIOR FILING DATE: 1998-12-14
17 <150> PRIOR APPLICATION NUMBER: 60/112,241
18 <151> PRIOR FILING DATE: 1998-12-14
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn version 3.0
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25 <211> LENGTH: 2075
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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38 gtgcacaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc gtg      171
39   Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val
40       1           5           10
42 gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc agc      219
43 Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser
44 15           20           25           30
46 ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg ggc      267
47 Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly
48           35           40           45
50 gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc aag      315
51 Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys
52           50           55           60
54 cag ctg ggc gag ctg tgc acc gag cgc gac ccc tgc gac ccg cac aag      363
55 Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys
56           65           70           75
58 ggc ctc ttc tgt gac ttc gcc tcc ccg gcc aac cgc aag atc ggc gtg      411
59 Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val
60           80           85           90
62 tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg tac      459
63 Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr
64 95           100           105           110
66 cgc agc gga gag tcc ttc cag agc agc tgc aag tac cag tgc acg tgc      507
67 Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys
68           115           120           125

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70 ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc atg gac gtt cgt 555
71 Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg
72 130 135 140
74 ctg ccc agc cct gac tgc gcc ttc ccg agg agg gtc aag ctg ccc ggg 603
75 Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly
76 145 150 155
78 aaa tgc tgc gag gag cgg gtg tgt gac gag ccc aag gac caa acc gtg 651
79 Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val
80 160 165 170
82 gtt ggg cct gcc ctg gcg gct tac cga ctg gaa gac acg ttt ggc cca 699
83 Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro
84 175 180 185 190
86 gac cca act atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg 747
87 Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp
88 195 200 205
90 agc gcc tgt tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc 795
91 Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr
92 210 215 220
94 aat gac aag gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg 843
95 Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met
96 225 230 235
98 gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa 891
99 Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys
100 240 245 250
102 aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt 939
103 Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu
104 255 260 265 270
106 tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta 987
107 Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val
108 275 280 285
110 tgt acc gac ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg 1035
111 Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro
112 290 295 300
114 gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg atg 1083
115 Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met
116 305 310 315
118 ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac 1131
119 Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp
120 320 325 330
122 atc ttt gaa tgc ctg tac tac agg aag atg tac gga gac atg gca 1176
123 Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
124 335 340 345
126 tgaagccaga gaggtagaga cattaactca ttagactgga acctgaaactg attcacatct 1236
128 catttttccg taaaatgat ttcagtagca caagttatgt aaatctgttt ttctaactgg 1296
130 gggaaaagat tcccacccaa ttcaaaacat tgtgccatgt caaacaata gtctatcttc 1356
132 ccagacact gggttgaaaga atgttaagac ttgacagtgg aactacatta gtacacagca 1416
134 ccagaatgta tattaaggtg tggctttagg agcagtggga gggtaaccggc ccggttagta 1476
136 tcatcagatc gactcttata cgagtaatat gcctgctatt tgaagtgtaa ttgagaagga 1536
138 aaatttttagc gtgctcactg acctgcctgt agccccagtg acagctagga tytgcatctt 1596

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142 acattctgat tcgaatgaca ctgttcagga atcggaatcc tgcgattag actggacagc 1716
144 ttgtggcaag tgaatttgcg tgaacaagc cagatttttt aaaaattata ttgtaaatat 1776
146 tgtgtgtgtg tgtgtgtgtg tttatatata tatatatgta cagttatcta agttaattta 1836
148 aagttgttgg tgccttttta ttttgtttt taatgctttg atatttcaat gttagcctca 1896
150 atttctganc accataggtg gaatgtaaag cttgtctgat cgttcaaagc atgaaatgga 1956
152 tacttatatg gaaattcttc tcagatagaa tgacagtcgg tcaaaacaga ttgtttgcaa 2016
154 agggagggca tcagtgtctt ggcaggctga ttctaggtg ggaaatgtgg tagctcacg 2075
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158 <211> LENGTH: 349
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160 <213> ORGANISM: Homo sapiens
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169 20 25 30
172 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
173 35 40 45
176 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
177 50 55 60
180 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
181 65 70 75 80
184 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
185 85 90 95
188 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
189 100 105 110
192 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
193 115 120 125
196 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
197 130 135 140
200 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
201 145 150 155 160
204 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
205 165 170 175
208 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
209 180 185 190
212 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
213 195 200 205
216 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
217 210 215 220
220 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
221 225 230 235 240
224 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
225 245 250 255
228 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
229 260 265 270
232 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
233 275 280 285

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236 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
237      290      295      300
240 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
241 305      310      315      320
244 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
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249      340      345
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263 Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
264 1      5      10      15
266 atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg agc gcc tgt      96
267 Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
268      20      25      30
270 tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc aat gac aac      144
271 Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
272      35      40      45
274 gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg gtc agg cct      192
275 Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
276      50      55      60
278 tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa aag tgc atc      240
279 Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
280 65      70      75      80
282 cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt tct ggc tgc      288
283 Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly Cys
284      85      90      95
286 acc agc atg aag aca tac cga gct aaa ttc tgt gga gta tgt acc gac      336
287 Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
288      100      105      110
290 ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg gtg gag ttc      384
291 Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
292      115      120      125
294 aag tgc cct gac ggc gag gtc atg aag aag aac atg atg ttc atc aag      432
295 Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile Lys
296      130      135      140
298 acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac atc ttt gaa      480
299 Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
300 145      150      155      160
302 tcg ctg tac tac agg aag atg tac gga gac atg gca tgaagccaga      526
303 Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
304      165      170

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306 gaggtagaga cattaactca ttagactgga acttgaactg attcacatct catttttccg 585
308 taataatgat ttccagtagca caagttatgt aaatctgttt ttctaactgg gggaaaagat 646
310 tcccaaccac ttcaaaacat tgtgccatgt caaacaata gtctatcttc cccaqacact 706
312 gggttgaaga atgttaagac tggacagtgg aactacatta gtacacagca ccagaatgta 766
314 tattaagggtg tggctttagg agcagtggga ggtaccggc cgggttagta tcatcagatc 826
316 gactcttata cgagtaataa gcctgctatt tgaagtgtaa ttgagaagga aaatttttagc 886
318 gtgctcactg acctgcccgt agccccagtg acagctagga tgtgcattct ccagccatca 946
320 agagactgag tcaagttgtt ccttaagtca gaacagcaga ctcagctctg acattctgat 1006
322 tgaatgaca ctgttcagga atcggaatcc tgcgattag actggacagc ttgtggcaag 1066
324 tgaatttgcc tgaacaagc cagatttttt aaaatttata ttgtaaatat tgtgtgtgtg 1126
326 tgtgtgtgtg tatatatata tatatatgta cagttatcta agttaattta aagttgtttg 1186
328 tgccttttta ttgtgtttl taatgctttg atatttcaat gttagcctca atttctgaac 1246
330 accataggta gaatgtaaag ctgtctgat cgttcaagc atgaaatgga tacttatatg 1306
332 gaaattctgc tcagatagaa tgacagtccg tcaaacaga ttgtttgcaa aggggaggca 1366
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338 <211> LENGTH: 172
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352 Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
353 35 40 45
356 Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
357 50 55 60
360 Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
361 65 70 75 80
364 Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly Cys
365 85 90 95
368 Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
369 100 105 110
372 Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
373 115 120 125
376 Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile Lys
377 130 135 140
380 Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
381 145 150 155 160
384 Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
385 165 170

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